

SEQUENCE LISTING

<110> UNIVERSITE DE LIEGE

<120> NUCLEOTIDE AND/OR AMINO-ACID SEQUENCE CONTROLLING THE
EXPRESSION OF A XYLANASE PROMOTER-OPERATOR NUCLEOTIDE
SEQUENCE

<130> P.ULG.18/WO

<140>

<141>

<160> 5

<170> PatentIn Ver. 2.1

<210> 1

<211> 969

<212> DNA

<213> Streptomyces sp.EC3

<220>

<221> CDS

<222> (127)..(933)

<400> 1

```

atctgcacgg tctcctcgcc gggggaaggg agtcgcaagg gccgggtgga cgcacggcta 60
cgcgcacgca gcgcgcgtcc cgacctatgg cctaaggtgt ctagagaagc gaggaggggt 120
taggga atg cct gct acc gac gac cgt cgg ccc aag tac cag cgg atc      168
      Met Pro Ala Thr Asp Asp Arg Arg Pro Lys Tyr Gln Arg Ile
          1             5                 10

gcg gac tct ttg cga gag gcg atc cag tcg ggc gag tac ggt ccc ggt      216
Ala Asp Ser Leu Arg Glu Ala Ile Gln Ser Gly Glu Tyr Gly Pro Gly
      15             20                 25                 30

gat cgg ctt ccc ggg gag aac gac ctc atg gcc acg cac ggc gtg gcc      264
Asp Arg Leu Pro Gly Glu Asn Asp Leu Met Ala Thr His Gly Val Ala
          35             40                 45

cgt atg acg gcc cgg cag gcg ctc ggc gtc ctg cgg gac gag ggc atc      312
Arg Met Thr Ala Arg Gln Ala Leu Gly Val Leu Arg Asp Glu Gly Ile
          50             55                 60

gcc gaa tcc cgg aag ggc gca ggt gtc ttc gtg cgg gcc ttc cgt ccg      360

```

Ala Glu Ser Arg Lys Gly Ala Gly Val Phe Val Arg Ala Phe Arg Pro	
65 70 75	
ctg cgc cga cgc ggc atc cag cgg ctg gcc cgc gac cag tgg ggc aac	408
Leu Arg Arg Arg Gly Ile Gln Arg Leu Ala Arg Asp Gln Trp Gly Asn	
80 85 90	
gga cgg tcc atc tgg tcg gcg gac atc gag gcc aga gac ctc cgg gtc	456
Gly Arg Ser Ile Trp Ser Ala Asp Ile Glu Ala Arg Asp Leu Arg Val	
95 100 105 110	
gac cag gtc tcg gtg ggc gag gag aaa gct ccc gag cac atc ggc gcg	504
Asp Gln Val Ser Val Gly Glu Glu Lys Ala Pro Glu His Ile Gly Ala	
115 120 125	
gtc ctg ggc atg gct gcc gaa gaa gtc gcg tgc gtg agg cgc cgg cgc	552
Val Leu Gly Met Ala Ala Glu Glu Val Ala Cys Val Arg Arg Arg Arg	
130 135 140	
ttc gtc ctg gac ggc aag ccg gtg ctg ctc gcg acg agt tac ctg ccc	600
Phe Val Leu Asp Gly Lys Pro Val Leu Leu Ala Thr Ser Tyr Leu Pro	
145 150 155	
ctg tcc ctg gtg gcc gga tcc gcc atc agc cga gag gac acc ggg ccg	648
Leu Ser Leu Val Ala Gly Ser Ala Ile Ser Arg Glu Asp Thr Gly Pro	
160 165 170	
ggc ggt acc tac gcc cgg ctt gcc gaa ctc ggc cac gaa ccg gtg cac	696
Gly Gly Thr Tyr Ala Arg Leu Ala Glu Leu Gly His Glu Pro Val His	
175 180 185 190	
ttc cgc gag gag atc cgc tca cgc atg ccg tcg ccg gac gag gtg aca	744
Phe Arg Glu Glu Ile Arg Ser Arg Met Pro Ser Pro Asp Glu Val Thr	
195 200 205	
cag ctg gac ctt gcc ccg ggc acc ccg gtc atc ctc atc tgc cgc acc	792
Gln Leu Asp Leu Ala Pro Gly Thr Pro Val Ile Leu Ile Cys Arg Thr	
210 215 220	
gcg ttc acc gac cag ggc cac cct gtc gag gtc aac gag atg acc ctg	840
Ala Phe Thr Asp Gln Gly His Pro Val Glu Val Asn Glu Met Thr Leu	
225 230 235	
gac gcc gct tcc tac gtc ttg gag tac gac ttc gac gcg ggc ccc gag	888
Asp Ala Ala Ser Tyr Val Leu Glu Tyr Asp Phe Asp Ala Gly Pro Glu	
240 245 250	
ccc gcc tcc ccc ggc gcc gac gcc aca gcg ccc gga gac ccg gcc	933

Pro Ala Ser Pro Gly Ala Asp Ala Thr Ala Pro Gly Asp Pro Ala
 255 260 265

tgacagcggg cgaccgttgg aagtctctgc atccccg

969

<210> 2

<211> 269

<212> PRT

<213> Streptomyces sp.EC3

<400> 2

Met Pro Ala Thr Asp Asp Arg Arg Pro Lys Tyr Gln Arg Ile Ala Asp
 1 5 10 15

Ser Leu Arg Glu Ala Ile Gln Ser Gly Glu Tyr Gly Pro Gly Asp Arg
 20 25 30

Leu Pro Gly Glu Asn Asp Leu Met Ala Thr His Gly Val Ala Arg Met
 35 40 45

Thr Ala Arg Gln Ala Leu Gly Val Leu Arg Asp Glu Gly Ile Ala Glu
 50 55 60

Ser Arg Lys Gly Ala Gly Val Phe Val Arg Ala Phe Arg Pro Leu Arg
 65 70 75 80

Arg Arg Gly Ile Gln Arg Leu Ala Arg Asp Gln Trp Gly Asn Gly Arg
 85 90 95

Ser Ile Trp Ser Ala Asp Ile Glu Ala Arg Asp Leu Arg Val Asp Gln
 100 105 110

Val Ser Val Gly Glu Glu Lys Ala Pro Glu His Ile Gly Ala Val Leu
 115 120 125

Gly Met Ala Ala Glu Glu Val Ala Cys Val Arg Arg Arg Arg Phe Val
 130 135 140

Leu Asp Gly Lys Pro Val Leu Leu Ala Thr Ser Tyr Leu Pro Leu Ser
 145 150 155 160

Leu Val Ala Gly Ser Ala Ile Ser Arg Glu Asp Thr Gly Pro Gly Gly
 165 170 175

Thr Tyr Ala Arg Leu Ala Glu Leu Gly His Glu Pro Val His Phe Arg
 180 185 190

Glu Glu Ile Arg Ser Arg Met Pro Ser Pro Asp Glu Val Thr Gln Leu
195 200 205

Asp Leu Ala Pro Gly Thr Pro Val Ile Leu Ile Cys Arg Thr Ala Phe
210 215 220

Thr Asp Gln Gly His Pro Val Glu Val Asn Glu Met Thr Leu Asp Ala
225 230 235 240

Ala Ser Tyr Val Leu Glu Tyr Asp Phe Asp Ala Gly Pro Glu Pro Ala
245 250 255

Ser Pro Gly Ala Asp Ala Thr Ala Pro Gly Asp Pro Ala
260 265

<210> 3
<211> 195
<212> DNA
<213> Streptomyces sp.EC3

<400> 3
cccaagtacc agcggatcgc ggactctttg cgagaggcga tccagtcggg cgagtacggt 60
cccgggtgatc ggcttccccg ggagaacgac ctcattggcca cgcacggcgt ggcccgtatg 120
acggcccggc aggcgctcgg cgtcctgcgg gacgagggca tcgccgaatc ccggaagggc 180
gcaggtgtct tcgtg 195

<210> 4
<211> 137
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: polylinker

<400> 4
agctaggcct atcgatggcg cgccaagcta gcaacttaag tagatctaac tagtctgcag 60
cagaagctta atatttaatt aagcggccgc agtactctcg agccgccatg ggcccgatat 120
cgtaccagg cctaatt 137

<210> 5
<211> 133
<212> DNA
<213> Streptomyces sp.EC3

<400> 5

agctaggcct atcgatggcg cgccaagcta gcaacttaag tagatctaac tagtctgcag 60
cagaagctta atatttaatt aagcggccgc agtactctcg agccgccatg ggcccgatat 120
cggtaccagg cct 133